FIG. 1A

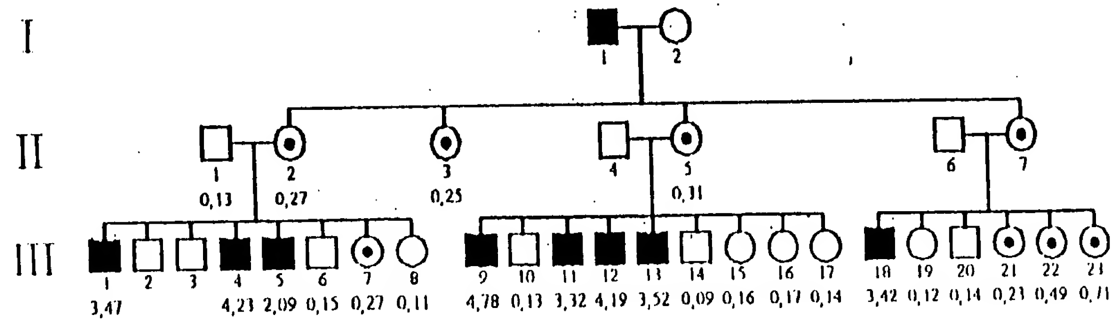


FIG. 1B

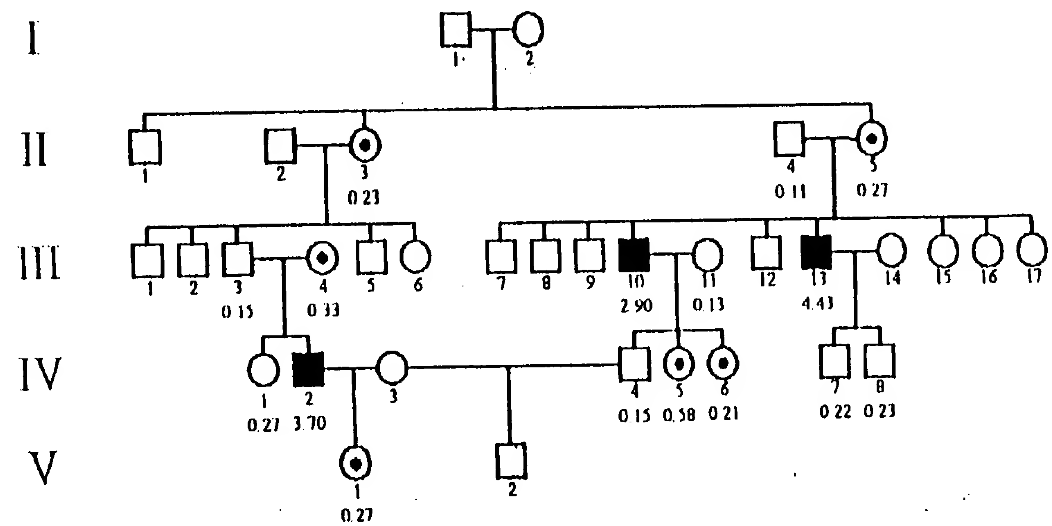
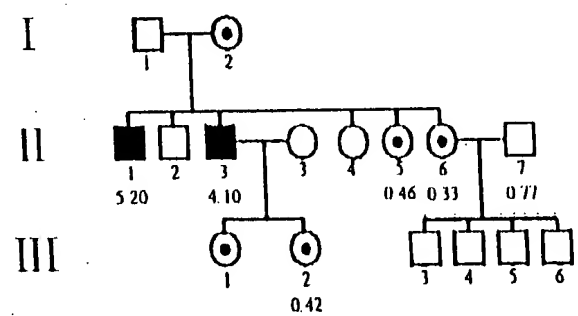


FIG. 1C



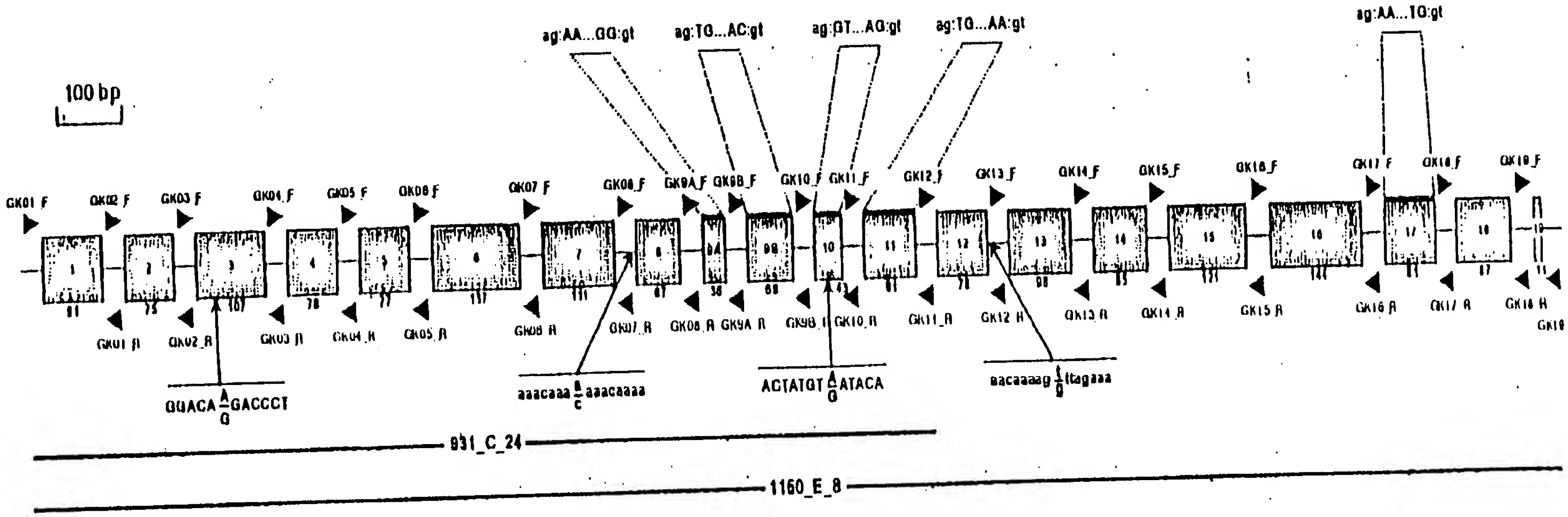
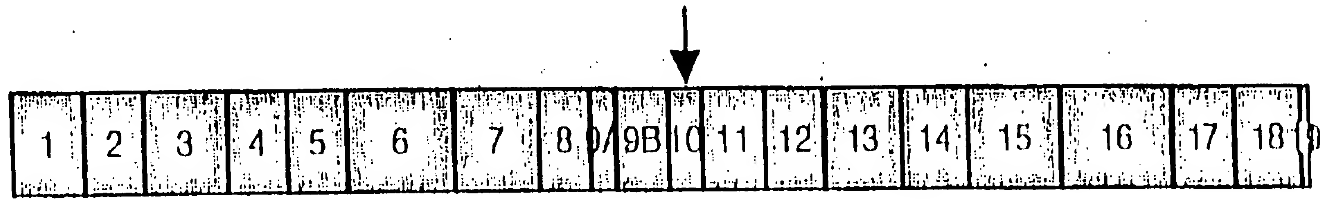

100 bp
ag:AA...GG:gt
ag:TG...AC:gt
ag:GT...AG:gt
ag:TG...AA:gt
ag:AA...TG:gt
GK01_F
GK02_F
GK03_F
GK04_F
GK05_F
GK06_F
GK07_F
GK08_F
GK9A_F
GK9B_F
GK10_F
GK11_F
GK12_F
GK13_F
GK14_F
GK15_F
GK16_F
GK17_F
GK18_F
GK19_F
GK01_R
GK02_R
GK03_R
GK04_R
GK05_R
GK06_R
GK07_R
GK08_R
GK9A_R
GK9B_R
GK10_R
GK11_R
GK12_R
GK13_R
GK14_R
GK15_R
GK16_R
GK17_R
GK18_R
GK19_R
GGACA $\frac{A}{G}$ GACCCT
aaacaaa $\frac{a}{c}$ aaacaaaa
ACTATGT $\frac{A}{G}$ ATACA
aacaaaag $\frac{t}{g}$ ttagaaa
931_C_24
1160_E_8

FIG. 2

000201"88046960

FIG. 3A

N288D



G TAT GGA ACA GGA TGT TTC TTA CTA TGT $\frac{A}{G}$ AT ACA GGC CAT AAG

FIG. 3B

	270 310	
GK N288D Mutant	FQIGQAKNTYGTGCFLLC**D**TGHKCVFSDHGLLTTVAYKLGR	SEQ ID NO: 6
glpk_human	FQIGQAKNTYGTGCFLLC**N**TGHKCVFSDHGLLTTVAYKLGR	SEQ ID NO: 7
glpk_rat	FQDGQAKNTYGTGCFLLC**N**TGHKCVFSEHGLLTTVAYKLGR	SEQ ID NO: 8
glpk_mouse	FQDGQAKNTYGTGCFLLC**N**TGHKCVFSEHGLLTTVAYKLGR	SEQ ID NO: 9
glpk_ecoli	VKEGMAKNTYGTGCFMLM**N**TGEKAVKSENGLLTTIAC--GP	SEQ ID NO: 10
glpk_pseae	VEPGQAKNTYGTGCFLLM**H**TGDKAVKSTHGLLTTIAC--GP	SEQ ID NO: 11
glpk_entca	FEKGMIKNTYGTGAFIVM**N**TGEEPQLSDNDLLTTIGY--GL	SEQ ID NO: 12
glpk_haein	VHAGQAKNTYGTGCFMLI**H**TGNKAITSKNGLLTTIACNAKG	SEQ ID NO: 13
glpk_bacsu	FEEGMGKNTYGTGCFMLM**N**TGEKAIKSEHGLLTTIAW--GI	SEQ ID NO: 14
glpk_yeast	YKPGAAKCTYGTGCFLLY**N**TGTKKLISQHGALTTLAFWFPH	SEQ ID NO: 15
glpk_mycge	TEPGMVKNTYGTGCFVLM**N**IGDKPTLSKHNLLTTVAWQLEN	SEQ ID NO: 16
glpk_entfa	FEPGMVKNTYGTGSFIVM**N**TGEEPQLSKNNLLTTIGY--GI	SEQ ID NO: 17
glpk_mycpn	VEPAMVKNTYGTGCFMLM**N**IGNELKYSQHNLLTTVAWQLEN	SEQ ID NO: 18
glpk_syny3	DRPGLLKCTYGTGAFLVA**N**TGQTVTRSQHRLLSTVAWTQTN	SEQ ID NO: 19

FIG. 4A

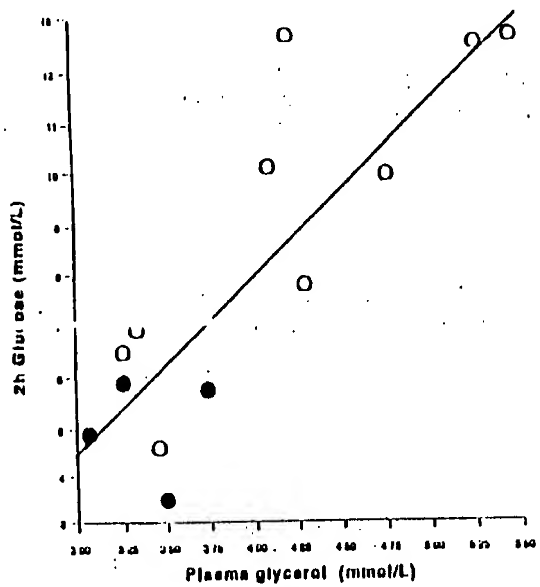


FIG. 4B

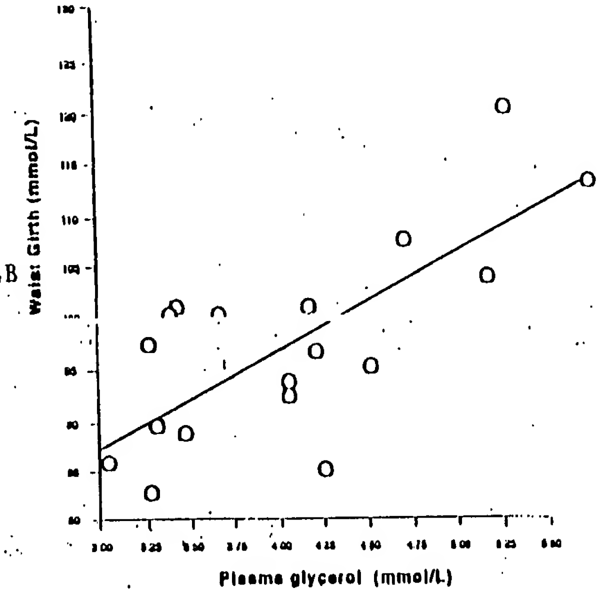


FIG. 4C

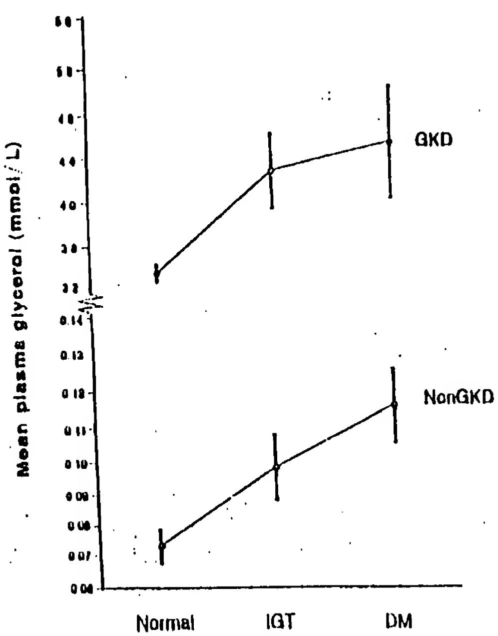
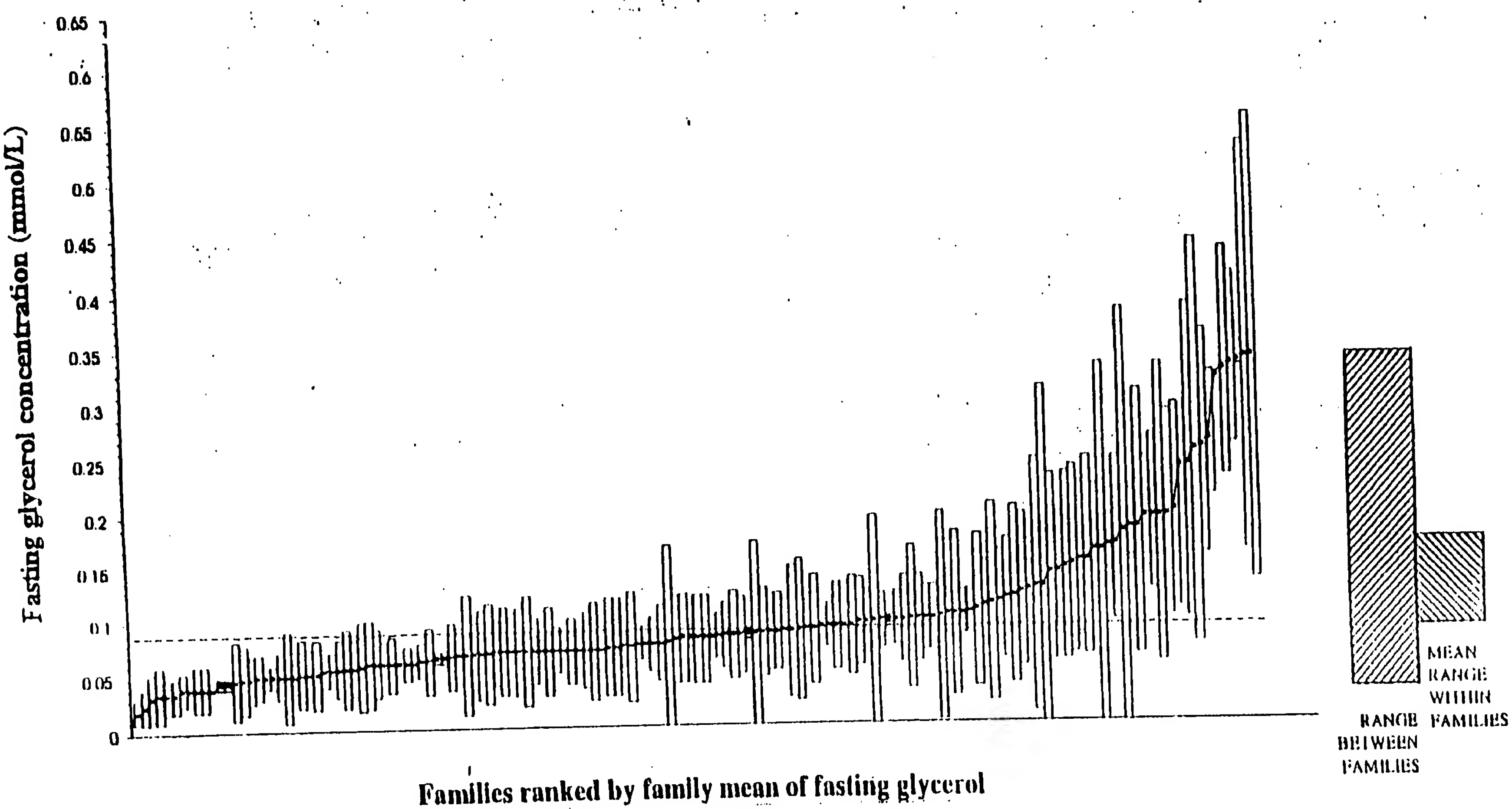


FIG. 5



Fasting glycerol concentration (mmol/L)
0.65
0.6
0.55
0.5
0.45
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
Families ranked by family mean of fasting glycerol
RANGE BETWEEN FAMILIES
MEAN RANGE WITHIN FAMILIES

poly: A/G
location:13th base of exon 3

ATGCCTTCTTTTGTCAAAGATGGGTGGAACA [A/G] GACCCTAAGGAAATTCTACAT
TCTGTCT SEQ ID NO: 1

CAA vs CAG ==> silent

poly: A/C
location:17th base of intron 8
TAATGGTAAAAAACAAACAAA [A/C] AAACAAAAAACACACCAAAAAACCAA

SEQ ID NO: 2

poly: A/G
location: 29th base of exon 10

TTCATTCTCCCTTCAACCATAGGTATGGAACAGGATGTTTCTTACTATGT [A/G] AT
ACAGGCCATAAGGTtGGTTTTTAATAAAAATGATTAAGTCA SEQ ID NO: 3

AAT vs GAT ==> N to D

poly: G/T
location: 22nd base of intron 12
GAAATTGGTGAGTGTGTTCTAACAAAAG [G/T] TTAGAAAATCTGAAAAATGACACA
TTTCA SEQ ID NO: 4

FIG. 6

SEQ ID NO: 5

Exon 1:
CCCTCCCCCTCCCCGCC
GGTTCAGCGGACGCGCGCGGCCTCGGTCTCTGGACTCGTCACCTGCCCCTCCCCCTCCCGCC
GCCGTCACCCAGGAAACCGGCCGCAATCGCCGGCCGACCTGAAGCTGGTTTCATGGCAGCCT
CAAAGAAGGCAGTTTTGGGGCCATTGGTGGGGGCGGTGGACCAGGGCACCAGTTCGACGCGC
TTTTTGGTGAGCCCGGGGTGACATGTGAAGAGGCGCTGAGC

Exon 2:
TGTAAAACGACGGCCAGTCATCCTTGATATCTGCCTGCATTTTTACATTAATATTACAATAT
CTTTTTCAGGTTTTCAATTCAAAAACAGCTGAACTACTTAGTCATCATCAAGTAGAAATAAA
ACAAGAGTTCCCAAGAGAAGGGTATGTTTCCTAATTTAATATGTAAAGACACATTATGTTTG
TTAGTCCATCTCACCCAACTTGCCC

Exon 3:
CAATGCCTTCTTTTGTCAAAGATGGGTGGAACA [A/G] GACCCTAAGGAAATTCTACATTCT
GTCTATGAGTGTATAGAGAAAACATGTGAGAAACTTGGACAGCTCAATATTGATATTTCCAA
CATAAAAGGTATTTTAGTAGAATATTTTACCCACA

Exon 4:
TGTAAAACGACGGCCAGTTGAGAGCTGTTTTCCTGAAGTAGTTCCTACTTGTTAAATTTTTG
ACTTCCTTCTGTTTAACTTTCTCTTTAAAGCTATTGGTGTCAGCAACCAGAGGGAAACCACT
GTAGTCTGGGACAAGATAACTGGAGAGCCTCTCTACAATGCTGTGGGTAAGCTGTCATGCAT
GGATGTCAAATGTAGGGCCTTTCTTCACATTGCAA

Exon 5:
TGTAAAACGACGGCCAGTTCCTTGATAGTGATTTCAGTAAGTTCTTATTTTTTTAAATGAAG
TTTTTCATGTATATTATTTTATTTTGGTCTATAGTGTGGCTTGATCTAAGAACCCAGTCTAC
CGTTGAGAGTCTTAGTAAAAGAATTCCAGGAAATAATAACTTTGTCAAGGTAAGAATTTCTT
CAGAAGTATACTATAAGAATGTTTCTTTTTTTAAAAAAAGTTTGCAGATTTCACTAGAAAGA
AGCATCTTATGGTACAATAGTTATTTGATACAATTTATAGAATCTTTTTCCCGGATAATTGA
GGCC

Exon 6:
TGTAAAACGACGGCCAGTTTCTTTTGTTTGGTGGTTTTGTTTTAAACTGTTACACTTTTCAT
TTGCTAACTGAACTTCACAACTGCTTTTAGTCCAAGACAGGCCTTCCACTTAGCACTTACTT
CAGTGCAGTGAAACTTCGTTGGCTCCTTGACAATGTGAGAAAAGTTCAAAAGGCCGTTGAAG
AAAAACGAGCTCTTTTTGGACTATTGATTCATGGCTTATTTGGGTATGTTTAAATATAATG
GATATATGGAGAATTTTTTCAGAAATTTTTTCTAGACTGCCTTGCCTATTGTTTCTACTAGC
AGGTCAGACTTTTTAATTAGCA

FIG. 7A

Exon 7:
TGTAAAACGACGGCCAGTTGTGCTCTGCTGATTATGACCCTTAACAATATGTAAATTAAATT
GCCAATAAGTACAAATTTAACCTGATTTTTTACTCTGCCTAGAGTTTGACAGGAGGAGTCA
ATGGAGGTGTCCACTGTACAGATGTAACAAATGCAAGTAGGACTATGCTTTTCAACATTCAT
TCTTTGGAATGGATAAACAACTCTGCGAGTAAGTTCTGTTTTGCTCTAAATATAGTTTTCC
CAATACACTACCTATTTATAACCGAAATCTTAATATTTTCAGATGTCAGTGGAGCA

Exon 8:
TGTAAAACGACGGCCAGTACAGTGTTAAATACCCAATCTTCTTGTTTTTCAGATTTTTTGGA
ATTCCAATGGAAATTCTTCCAAATGTCCGGAGTTCTTCTGAGATCTATGGCCTAATGGTAAA
AAACAAACAAA [A/C] AAACAAAAAACACACCAAAAAACCAAAAAACAAACAAAAAAAAACC
TAATAATTAAAGTTTTTTTATTACAAAACAAGTTTACTATTCATAATTCAAAAGTCAACTGT
GTTATGTTTTGTGACTTAAAAACTTTACAGTCCTTTTTACAATGG

Exons 9A and 9B
AAAGCTGGGGCCTTGGAAGGTGTGCCAATATCTGGGGTAAGTTTCATCACCAAGTGTCTCCC
CATCCCCACCCTTCCCCATGTTATGGCTTTCCTCCTCTTAGTTCATCAGTGTGCCTCTTTTT
AAACTAGGGAAAACAAGTAAAAGTTGCAAAATTGGANNNNTCTTGTTCTTACATGTCATACT
GTGGGCCATTGAGAATCTTTTGAATAAATTAATTTTAACTCTCCCTTCCCATACCTATTATC
TTACATATTAACAAATGGTATTAACAAATGGGGAAAATGGCCAAATGGAGAAAATGCAAGGA
AATAGACAGTTCATTCTTTGATAAATAAAAAATGAAAAATAAATCCTATGGCTCTTCTAAAA
AGAAAGTTAATACTATTGTATTAGTCAGTGTTCTTTATTGTCATTTATACTTTCAGTGTTTA
GGGGACCAGTCTGCTGCATTGGTGGACAAATGTGCTTCCAGATTGGACAAGCCAAAAATAC
GTGAGTTTAAGAAACAGACTTAAAAACCAATGCTGTTTTGTTTTTTCTACTTGGTGCTTTGA
ATAAGGAAAAGCTTTTGAAGTTCATCCAGGATGAAAATCAATAGCTTAATAGCTCCAATATG
CATATATACACTTTTTACCATTTTTTTATATCTTTAAATAAAATACAAAA
TGCCATATATATGCACACTGATGAAGCTTATAAAGACCTAAATTTGTAGGCTGGGCGCGG

Exons 10 and 11:
TTATTTGCTTTCAATAAAATTGTCTTCTATTCATTCTCCCTTCAACCATAGGTATGGAACAG
GATGTTTCTTACTATGT [A/G] ATACAGGCCATAAGGTTGGTTTTTTAAATTAAAAAATTGA
TTTAAAAGTCTAAGTTCATCTAAATAATGCTTGAACATAATTTACTATTAAACAACTTTTAG
TCTTTAGCTTTTACTTAATCTTTATCAGGGTTTAATTTAGAGCTCAATACAAAATTTGAATC
GTTCTAATAAGAACCATTTTAGACTCTTTGAATTTTATATGTGTGTTTTTAATTGTGCTGGG
GGGAAATCTAGACTGAGACCTCATCAAATTCTTAATGCAAATCTAATTTGAAACAAGGAATA
AACTTTTTATACAGCTTAAATGTGTTCTTAATTCTGATCGTTTTGACTGTAAGGATTTATTT
TAAAAATTGGTTTATTGATTGCATTATTTTGTACCTATGTTATTTTAACTTTAAAAAAAAGT
TCTCATGTTATCTTTTCATTTTCCACTACTGAAATCTTTTTTTTTTCTTTCTTACAGTGTGT
ATTTTCTGATCATGGCCTTCTCACCACAGTGGCTTACAAACTTGGCAGAGACAAACCAGTAT
ATTATGCTTTGGAAGTAAGTTCTTTTTAATCAATATGGATAATATGACAAACATTCAAAGCT
AATAAAAATCACAGAGTTTTCTAACACTTTTCTGGTAAATCTTAATACAGAGGACTCAAAAA
GTTCTGCTTTCTTGGCATTTGATTGAGTTGAAGGAACCTGAAACTGATCTGGGTGTCAGGAC
TCACAGGAGACCTTGATTAGATTGGTTCCTCAGTTCTTATGCCAATTAATCATGTCACCTTA
GGCATATTACTTGAGAGCTCTACAATGTGAGGTTTTTTTTTTTTTTATCTCTAAAGTTTAAT
CGGATTAACGTGCTCTCTAACATTTCTTTCATCTTGAAAATTCTTTGATTTTATAAATAAAA
TGCTCCAGTGTTCCAAAGAGAACCCTGGGCACAAATAGGCAGAACAACTCTCTTCACTTGTC
TCCTCATAAAAATAAATTTTGTGTAACATTTTGATATAGAAAAGAAAGCGACGAGATTTATG
CCACTTATCACTGGAAACATTTGTTTCAAACATTTTTGTATGTTATAGTAGGAATATGCCAG
CCTAAGCCTATA

FIG. 7B

Exon 12:
TTTTATTAGTGACTTAGATAAAACTATGTTTGTATTAGAAGACCTAGTTTACATATTTGTCG
GAGTCTCAAAATGGAAACTGAATTCTGTCCATCTGATTGTGTCATACACAGAATATGCTCAA
TAAAAACCTTGGATAGTGATAAAATATATTCTGTCTTGAATTCCTTTTTTTCTTTAGGGTTC
TGTAGCTATAGCTGGTGCTGTTATTCGCTGGCTAAGAGACAATCTTGGAATTATAAAGACCT
CAGAAGAAATTGGTGAGTGTGTTCTAACAAAAG [G/T] TTAGAAAATCTGAAAAATGACACA
TTTCAGTATTTTATCTCTGCAAAGTAAATATCGATGCTTTGCCCCAAATGTGAT

Exon 13:
CCAGTTGTGTGATTTTTGTTTTGTTTTGTTTTAATGTTAGAAAAACTTGCTAAAGAAGTAGG
TACTTCTTATGGCTGCTACTTCGTCCCAGCATTTTCGGGGTAATATGCACCTTATTGGAGC
CCAGCGCAAGAGGGTAAGTATTGAAAATATGGAGTGCTTTTGGGGATCTTGATTTAT

Exons 14 and 15:
TGTAAAACGACGGCCAGTTGATTATGTCCAATTTTCTCTTCCTGGACATTTCTGTCTACCAA
ATTTGACCTTTTCATATTTGAGATATTTCAAATTGATTGGTTTATATCATTCTAATCTGAAA
ATCTTTGTGCGTATTTTTAGGATAATCTGTGGACTCACTCAGTTCACCAATAAATGCCATAT
TGCTTTTGCTGCATTAGAAGCTGTTTGTTTCCAAACTCGAGAGGTAACAAATATGGCCTGT
TTTCTTGTACTTAGTTCACTTTTATCACTCTTAAGTTATATGTTAACACCCGAGATTTATTC
AGTACTGAAAATGTAGTTAATCAAATATTAAGGCTGCCTAAATACTAATCTAAATATAAGCA
GGGTTTTCCCCCTTTTTCCAGCTGTCATTACCTTCTAAGTTCCTGTTCCCTGTCAGGCACTG
GGAAATTTATGGTTGTGGGAGGCTGAGTGGCACACATTAGGCAAAGGAAACAGCACAAACA
TAGGCATCaAGGCAGAAAAACAGGGTGCAAAATAGAGTTGTATAGCTTAGCTGAATATCAAG
GTGAATGCAGAGGTGTAGTGAGAGAAAAGGTTGGCTGTGACCAGATCAAAGAGGGCTTAGAA
GACCAGAATAAGAAGTCTCAATTTATTCCATAGGCTCTTGGAAGCTCTTGAGAGTTTCTGAG
TGGAGGATTGCCATTTTCAGAGATGTTACTATGAAATAGATTTATAACATTAATTGCACTGG
TTTATTTAAGATTTTGGATGCCATGAATCGAGACTGTGGAATTCCACTCAGTCATTTGCAGG
TAGATGGAGGAATGACCAGCAACAAAATTCTTATGCAGCTACAAGCAGACATTCTGTATATA
CCAGTAGGTTAGTAAGTCTTCATTCCTTTAAACTCCCAGAGTAATGTTTCTTGTGGAATAAC
TAGTTCTTTGGG

Exon 16:
TGTAAAACGACGGCCAGTTCCCAGAGTAATGTTTCTTGTGGAATAACTAGTTCTTTGGCAT
ATGTAACCACAAAGATATTGATGGAACTCTCTCTCCTCAGTGAAGCCCTCAATGCCCGAAAC
CACTGCACTGGGTGCGGCTATGGCGGCAGGGGCTGCAGAAGGAGTCGGCGTATGGAGTCTCG
AACCCGAGGATTTGTCTGCCGTCACGATGGAGCGGTTTGAACCTCAGATTAATGCGGAGGGT
ACATTTAAAGAATGAAATGTTCAGTGATATACTGTGAAAACGACCTTAGTGCACGGGAGTTT
TGTTTTTCTGTTTAGTTAAAAGTTAAGGAACCAAGTAAAATAGTAAATGTTATCATTGCAGA
TTCGGCTGCCAAGCATATTGGGCTTTACTGAATAAATGTGAATGAGAGAAATCGTTGCTTAT
CAAAAGAACTTCTAAAATCACTTTTTAAAAATCATT

Exon 17:
TGTAAAACGACGGCCAGTAGCCCTACTGCAGTTTAATGTGTCAATAATTTGTCAAGAATGTT
GAGTGATCATAAGTATGGTACTAAGAACATCTCAGCAAACTACCTTTCGTTATGTGTTTTTT
CTACCTTCTAATTCTAGAAAGTGAAATTCGTTATTCTACATGGAAGAAAGCTGTGATGAAGT
CAATGGGTTGGGTTACAACTCAATCTCCAGAAAGTGGTAAAAATGTTTTTGTTTATTATTGT
CACATTTTCTTAGTATATTAAATAGTTATTTAAGTATCTAGGCATTTACACATAGCCAGGCT
GCTCTGAAGAAAAGCATTATCATATGTCCAGAGATTCTGACATTTTGAAAACACTTTAAAGT
TCTAAACACAAAATGTAAATTATCAGGTGT

FIG. 7C

Exon 18:
TGTAAAACGACGGCCAGTTGGTTTGGTTTGCTTGACTGGAATCTCTTCTGCTTGGATGACCA
CAGGTGACCCTAGTATCTTCTGTAGTCTGCCCTTGGGCTTTTTATAGTGAGTAGCATGGTA
ATGTTAATCGGAGCAAGGTACATCTCAGGTTAGTTACTCTTTAAATTAGACAACTCTATTAG
TTAGCTTTAATGTTTTCGTGTATAACTTAGCAGAAATTTTTCAGTGTTTTTCATTCTTTCTG
TGTCTAGGAAGCTGGAAAATCAATTAAAGGTCTAATTAGTTAGACCAATTAATCTTTGGGGG
CAGTTAGAAGTAAGAACTGTGACTCTGCTTACCCTTTTTAAATTTTTAATGTGATGACTTCT
TTAAGAGGGACTACATTCTGCTGTCAGCTGCAGCAATAAGCAAAAGTGAAAATACTAATATT
TAAATGACAGGACTTTCAGACTGACTGCTGAAAGTTAAAGTATACTT

Exon 19:
AAAATTACTGGCTTAAATGGAAATGATGCTTCTTATTCTGTATGTTCCCATGAAAGTGAAAC
TTAAAAAAAAAATTCATGATTAGGGTTTCATGAAAAGGCCTTGTTTCTATGAAAATTGAGAC
AGGTTGCATCTCTCTAAGCTAAAAGATGGGCTATGTGTCTAGAGTCTTAGACTTCTAAAATG
CATGTGGTCACTATATGTAGGTTATCTCTTCGGTGACATACACTGCAATTTGAGAGGGCTGG
AAATTGTTTGCCTTGGTAAACGATTAGCAACAGTGGCAATATTTGTTAATTTTGGAATTGGC
CCTGTTTGTTGCATTTTAATTGTGAGGCATGATTTAGAAATCATATGGACTTTCTAGCTTAA
TAAATGATTGAATCATCTGCATTGCTTTAACTCCTGAATTGTATGCATGTATTATTGACATA
TATGGTTTTTGTTCCCCATTTCAGGTATTCCATAAAACCTACCAACTCATGGATTCCCAAGA
TGTGAGCTTTTTACATAATGAAAGAACCCAGCAATTCTGTCTCTTAATGCAATGACACTATT
CATAGACTTTGATTTTATTTATAAGCCACTTGCTGCATGACCCTCCAAGTAGACCTGTGGCT
TAAAATAAAGAAAATGCAGCAAAAAGAATGCTATAGAAATATTTGGTGGTTTTTTTTTTTTT
TAAACATCCACAGTTAAGGTTGGGCCAGCTACCTTTGGGGCTGACCCCCTCCATTGCCATAA
CATCCTGCTCCATTCCCTCTAAGATGTAGGAAGAATTCGGATCCTTACCATTGGAATCTTCC
ATCGAACATACTCAAACACTTTTGGACCAGGATTTGAGTCTCTGCATGACATATACTTGATT
AAAAGGTTATTACTAACCTGTTAAAAATCAGCAGCTCTTTGCTTTTAAGAGACACCCTAAAA
GTCTTCTTTTCTACATAGTTGAAGACAGCAACATCTTCACTGAATGTTTGAATAGAAACCTC
TACTAAATTATTAAAATAGACATTTAGTGTTCTCACAGCTTGGATATTTTTCTGAAAAGTTA
TTTGCCAAAACTGAAATCCTTCAGATGTTTTCCATGGTCCCACTAATTATAATGACTTTCTG
TCTGGGTCTTATAGGAAAAGATACTTTCTTTTTTCTTCCATCTTTCCTTTTTATATTTTTTA
CTTTGTATGTATAACATACATGCCTATATATTTTATACACTGAGGGAGCCCATTTATAAATA
AAGAGCACATTATATTCAGAAGGTTCTAACAGGG

FIG. 7D

TABLE 1

Characteristics of carriers of the N288D GK gene mutation and of their unaffected relatives

	Men			Women		
	N288D carriers	Unaffected relatives	p	N288D carriers	Unaffected relatives	p
N	18	18		14	14	
Age (years)	46,4±14,2	42,0±18,8	0.32	44,9±13,5	43,7±17,8	0.87
Uncorrected triglyceride (mmol/L)[(1)]	6,26±1,13	2,05±0,54	<0,0001	2,84±1,20	1,30±0,65	0.0002
Glycerol (mmol/L)	3,99±0,71	0,10±0,04	<0,0001	0,54±0,14	0,10±0,02	<0,0001
Corrected triglyceride (mmol/L)[(1)]	2,27±0,75	1,95±0,53	<0,0001	2,31±1,22	1,19±0,67	0.03
Free fatty acid (mmol/L)	0,77±0,22	0,57±0,25	0.01	1,29±0,35	0,76±0,17	0.0004
Fasting glucose (mmol/L)	5,2±0,74	4,8±0,31	0.13	5,0±0,7	4,6±0,3	0.10
2h glucose following OGTT (mmol/L)	7,9±3,1	5,8±1,6	0.02	7,0±6,1	5,0±2,1	0.04
Fasting insulin (mU/L)[(1)]	13,3±14,0	15,1±14,8	0.62	12,2±13,1	9,0±3,4	0.60
Waist girth (cm)	97,7±9,3	88,1±12,3	0.01	88,5±3,8	79,3±5,8	0.03
Body mass index (kg/m^2)	27,9±4,1	24,9±3,9	0.03	28,1±5,5	23,1±2,3	0.001
% total body fat	27,1±7,2	22,9±7,6	0.01	46,3±3,1	33,9±11,3	0.001

(1) geometric mean, p value after log transformation

Figure 8

TABLE 2

Fasting plasma glycerol concentration (mmol/L) in the initial cohort of 1056 individuals, by risk factor of glucose intolerance and diabetes mellitus

			No.	Glycerol geometric mean ± SD	p
Gender					
	men		717	0.065 ± 0.081	
	women	- premenopaused	137	0.071 ± 0.093	<0.0001
		- menopaused	202	0.099 ± 0.085	
Age (Y)					
		<50	486	0.071 ± 0.082	
		50 - 60	408	0.076 ± 0.106	0.0015
		>60	165	0.083 ± 0.053	
Fasting glucose (mmol/L)					
		< 5.2	449	0.068 ± 0.080	
		5.2 - 5.9	336	0.070 ± 0.090	<0.0001
		6.0 - 6.9	271	0.090 ± 0.100	
Fasting insulin (UI)					0.02
		<15	637	0.067 ± 0.082	
		≥15	419	0.086 ± 0.101	
2 hours glucose (mmol/L)					
		<7.8	572	0.062 ± 0.071	
		7.8 - 11.0	283	0.081 ± 0.101	<0.0001
		≥11.1	201	0.102 ± 0.110	
Triglyceride (mmol/L)					<0.0001
		≤ 2.2	389	0.057 ± 0.062	
		>2.2	667	0.082 ± 0.103	
Free fatty acid (mmol/L)					<0.0001
		< 0.6	589	0.066 ± 0.054	
		≥0.6	467	0.111 ± 0.112	
Body mass index (kg/m2)					<0.0001
		≤ 27	428	0.060 ± 0.087	
		>27	628	0.079 ± 0.097	

p value from one-way ANOVA

Figure 9

TABLE 3. Multivariate analysis of the relationships of fasting plasma glycerol concentration with impaired glucose tolerance (2h glucose 7,8-11,0 mmol/L following a 75 g oral load) before and after adjustment for covariates identified in

	Model 1	Model 2	Model 3	Model 4
Glycerol (log)				
ß	1.75	1.62	1.46	0.7[illegible]
Odds ratio	5.76	5.42	4.33	2.4[illegible]
p	<0.0001	<0,0001	<0,0001	0.0[illegible]
Triglyceride (log)				
ß		0.54	0.35	0.1[illegible]
Odds ratio		1.75	1.42	1.1[illegible]
p		0.02	0.11	0.6[illegible]
Body mass index (kg/m²)				
ß			0.10	0.0[illegible]
Odds ratio			1.10	1.0[illegible]
p			<0.0001	0.0[illegible]
Fasting insulin (log)				
ß				0.[illegible]7
Odds ratio				1.[illegible]
p				0.[illegible]9
Fasting glucose (mmol/L)				
ß				1.1[illegible]
Odds ratio				2.[illegible]5
p				<0,0001
Free fatty acid (log)				
ß				1.[illegible]2
Odds ratio				4.[illegible]3
p				0.0[illegible]7

Odds ratios are expressed as the increase in the risk of 2h glucose ≥7,8 mmol/L following a 75 g oral charge, associated with a 1-SD increase in the variables studied. ß denotes the standardized estimate which is the parameter estimate of each variable in the multivariate logistic model. All models included age and gender as covariates. Otherwise, only the variables included in each model are shown. Subjects with severe hyperglycemia due to the N788D mutation in the

Figure 10